

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/612,852
 DATE: 05/21/2001
 TIME: 11:54:00

Input Set : A:\Pto.amc
 Output Set: N:\CRF3\05212001\I612852.raw

```

3 <110> APPLICANT: Curiel, David T.
4   Krasnykh, Victor N.
6 <120> TITLE OF INVENTION: Modified Adenovirus Containing A Fiber
7   Replacement Protein
W--> 8 <130> FILE REFERENCE: D6070CIP
W--> 9 <140> CURRENT APPLICATION NUMBER: US/09/612,852
9 <141> CURRENT FILING DATE: 2000-07-10
10 <150> PRIOR APPLICATION NUMBER: US 09/250,580
11 <151> PRIOR FILING DATE: 1999-02-16
12 <150> PRIOR APPLICATION NUMBER: US 60/074,844
13 <151> PRIOR FILING DATE: 1998-02-17
W--> 14 <160> NUMBER OF SEQ ID: 14
16 <210> SEQ ID NO: 1
17 <211> LENGTH: 40
18 <212> TYPE: DNA
19 <213> ORGANISM: artificial sequence
W--> 20 <220> FEATURE:
21 <221> NAME/KEY: primer_bind
22 <223> OTHER INFORMATION: Forward primer FF.F used to amplify segment of the T4
23   fibritin gene encoding amino acids Ser-229 through
24   the carboxy terminal Ala-487.
W--> 25 <400> SEQUENCE: 1
26 ggggaacttga cctcacagaa cgtttatagt cgtttaaagt      40
28 <210> SEQ ID NO: 2
29 <211> LENGTH: 37
30 <212> TYPE: DNA
31 <213> ORGANISM: artificial sequence
W--> 32 <220> FEATURE:
33 <221> NAME/KEY: primer_bind
34 <223> OTHER INFORMATION: Reverse primer FF.R used to amplify segment of the T4
35   fibritin gene encoding amino acids Ser-229 through
36   the carboxy terminal Ala-487.
W--> 37 <400> SEQUENCE: 2
38 aggccatggc caatttttgc cggcgataaa aaggtag      37
40 <210> SEQ ID NO: 3
41 <211> LENGTH: 53
42 <212> TYPE: DNA
43 <213> ORGANISM: artificial sequence
W--> 44 <220> FEATURE:
W--> 45 <221> NAME/KEY:
46 <223> OTHER INFORMATION: synthetic oligo, F5._3Swa.T, for the introduction of
47   SwaI restriction site
W--> 48 <400> SEQUENCE: 3
49 ttggcccat ttaatgaat cgtttgtgtt atgtttcaac gtgtttattt ttc      53
51 <210> SEQ ID NO: 4
52 <211> LENGTH: 61
53 <212> TYPE: DNA

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54 <213> ORGANISM: artificial sequence
W--> 55 <220> FEATURE:
W--> 56 <221> NAME/KEY:
57 <223> OTHER INFORMATION: synthetic oligo, F5._3Swa.B, for the introduction of
58     SwaI restriction site
W--> 59 <400> SEQUENCE: 4
60 aattgaaaaa taaacacggt gaaacataac acaaacgatt catttaaagt 50
61 gggccaatat t 61
63 <210> SEQ ID NO: 5
64 <211> LENGTH: 57
65 <212> TYPE: DNA
66 <213> ORGANISM: artificial sequence
W--> 67 <220> FEATURE:
W--> 68 <221> NAME/KEY:
69 <223> OTHER INFORMATION: synthetic oligo, FFBLL.T
W--> 70 <400> SEQUENCE: 5
71 ggcaggtgga ggcggttcag gcggaggtgg ctctggcgggt ggcggatccg 50
72 gggattt 57
74 <210> SEQ ID NO: 6
75 <211> LENGTH: 57
76 <212> TYPE: DNA
77 <213> ORGANISM: artificial sequence
W--> 78 <220> FEATURE:
W--> 79 <221> NAME/KEY:
80 <223> OTHER INFORMATION: synthetic oligo, FFBLL.B
W--> 81 <400> SEQUENCE: 6
82 aaatcccgg atccgccacc gccagagcca cctccgcctg aaccgcctcc 50
83 acctgcc 57
85 <210> SEQ ID NO: 7
86 <211> LENGTH: 36
87 <212> TYPE: DNA
88 <213> ORGANISM: artificial sequence
W--> 89 <220> FEATURE:
W--> 90 <221> NAME/KEY:
91 <223> OTHER INFORMATION: synthetic oligo, RGS6H.T
W--> 92 <400> SEQUENCE: 7
93 gatctagagg atcgcatcac catcaccatc actaat 36
95 <210> SEQ ID NO: 8
96 <211> LENGTH: 32
97 <212> TYPE: DNA
98 <213> ORGANISM: artificial sequence
W--> 99 <220> FEATURE:
W--> 100 <221> NAME/KEY:
101 <223> OTHER INFORMATION: synthetic oligo, RGS6H.B
W--> 102 <400> SEQUENCE: 8
103 attagtgatg gtgatggtga tgcgatcctc ta 32
105 <210> SEQ ID NO: 9
106 <211> LENGTH: 27
107 <212> TYPE: DNA

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108 <213> ORGANISM: artificial sequence
W--> 109 <220> FEATURE:
110 <221> NAME/KEY: primer_bind
111 <223> OTHER INFORMATION: primer to PCR amplify FF/6H in pXK.FF/6H
W--> 112 <400> SEQUENCE: 9
113 ccctcatgaa gcgcgcaaga ccgtctg          27
115 <210> SEQ ID NO: 10
116 <211> LENGTH: 27
117 <212> TYPE: DNA
118 <213> ORGANISM: artificial sequence
W--> 119 <220> FEATURE:
120 <221> NAME/KEY: primer_bind
121 <223> OTHER INFORMATION: primer to PCR amplify FF/6H in pXK.FF/6H
W--> 122 <400> SEQUENCE: 10
123 cccaagctta gtgatggtga tggatg          27
125 <210> SEQ ID NO: 11
126 <211> LENGTH: 8
127 <212> TYPE: PRT
128 <213> ORGANISM: Adenovirus type 5
W--> 129 <220> FEATURE:
130 <221> NAME/KEY: DOMAIN
131 <223> OTHER INFORMATION: the beginning of the third pseudorepeat of the
132     fiber shaft domain
W--> 133 <400> SEQUENCE: 11
134 Gly Asn Thr Leu Ser Gln Asn Val
135     5                      8
137 <210> SEQ ID NO: 12
138 <211> LENGTH: 26
139 <212> TYPE: PRT
140 <213> ORGANISM: Phage T4
W--> 141 <220> FEATURE:
142 <221> NAME/KEY: DOMAIN
143 <223> OTHER INFORMATION: the sixth coiled coil segment of the __-helical
144     central domain of the fibritin
W--> 145 <400> SEQUENCE: 12
146 Val Tyr Ser Arg Leu Asn Glu Ile Asp Thr Lys Gln Thr Thr Val
147     5                      10                      15
148 Glu Ser Asp Ile Ser Ala Ile Lys Thr Ser Ile
149     20                      25
151 <210> SEQ ID NO: 13
152 <211> LENGTH: 361
153 <212> TYPE: PRT
154 <213> ORGANISM: artificial sequence
W--> 155 <220> FEATURE:
156 <221> NAME/KEY: CHAIN
157 <223> OTHER INFORMATION: the fiber-fibritin-6H chimera
W--> 158 <400> SEQUENCE: 13
159 Met Lys Arg Ala Arg Pro Ser Glu Asp Thr Phe Asn Pro Val Tyr
160     5                      10                      15

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```

161 Pro Tyr Asp Thr Glu Thr Gly Pro Pro Thr Val Pro Phe Leu Thr
162                20                25                30
163 Pro Pro Phe Val Ser Pro Asn Gly Phe Gln Glu Ser Pro Pro Gly
164                35                40                45
165 Val Leu Ser Leu Arg Leu Ser Glu Pro Leu Val Thr Ser Asn Gly
166                50                55                60
167 Met Ala Leu Lys Met Gly Asn Gly Leu Ser Leu Asp Glu Ala Gly
168                65                70                75
169 Asn Leu Thr Ser Gln Asn Val Tyr Ser Arg Leu Asn Glu Ile Asp
170                80                85                90
171 Thr Lys Gln Thr Thr Val Glu Ser Asp Ile Ser Ala Ile Lys Thr
172                95                100               105
173 Ser Ile Gly Tyr Pro Gly Asn Asn Ser Ile Ile Thr Ser Val Asn
174                110               115               120
175 Thr Asn Thr Asp Asn Ile Ala Ser Ile Asn Leu Glu Leu Asn Gln
176                125               130               135
177 Ser Gly Gly Ile Lys Gln Arg Leu Thr Val Ile Glu Thr Ser Ile
178                140               145               150
179 Gly Ser Asp Asp Ile Pro Ser Ser Ile Lys Gly Gln Ile Lys Asp
180                155               160               165
181 Asn Thr Thr Ser Ile Glu Ser Leu Asn Gly Ile Val Gly Glu Asn
182                170               175               180
183 Thr Ser Ser Gly Leu Arg Ala Asn Val Ser Trp Leu Asn Gln Ile
184                185               190               195
185 Val Gly Thr Asp Ser Ser Gly Gly Gln Pro Ser Pro Pro Gly Ser
186                200               205               210
187 Leu Leu Asn Arg Val Ser Thr Ile Glu Thr Ser Val Ser Gly Leu
188                215               220               225
189 Asn Asn Asp Val Gln Asn Leu Gln Val Glu Ile Gly Asn Asn Ser
190                230               235               240
191 Thr Gly Ile Lys Gly Gln Val Val Ala Leu Asn Thr Leu Val Asn
192                245               250               255
193 Gly Thr Asn Pro Asn Gly Ser Thr Val Glu Glu Arg Gly Leu Thr
194                260               265               270
195 Asn Ser Ile Lys Ala Asn Glu Thr Asn Ile Ala Ser Val Thr Gln
196                275               280               285
197 Glu Val Asn Thr Ala Lys Gly Asn Ile Ser Ser Leu Gln Gly Asp
198                290               295               300
199 Val Gln Ala Leu Gln Glu Ala Gly Tyr Ile Pro Glu Ala Pro Arg
200                305               310               315
201 Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu
202                320               325               330
203 Ser Thr Phe Leu Ser Pro Ala Gly Gly Gly Gly Ser Gly Gly Gly
204                335               340               345
205 Gly Ser Gly Gly Gly Gly Ser Arg Gly Ser His His His His His
206                350               355               360
207 His
208 361
210 <210> SEQ ID NO: 14

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211 <211> LENGTH: 9
212 <212> TYPE: PRT
213 <213> ORGANISM: Unknown
W--> 214 <220> FEATURE:
215 <221> NAME/KEY: DOMAIN
216 <223> OTHER INFORMATION: a peptide ligand containing the RGD motif
W--> 217 <400> SEQUENCE: 14
218 Cys Asp Cys Arg Gly Asp Cys Phe Cys
219 5 9

VERIFICATION SUMMARY

DATE: 05/21/2001

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TIME: 11:54:01

Input Set : A:\Pto.amc

Output Set: N:\CRF3\05212001\I612852.raw

L:8 M:283 W: Missing Blank Line separator, <130> field identifier
L:9 M:282 W: Numeric Field Identifier Missing, <140> CURRENT APPLICATION NUMBER: is Added.
L:14 M:283 W: Missing Blank Line separator, <160> field identifier
L:20 M:283 W: Missing Blank Line separator, <220> field identifier
L:25 M:283 W: Missing Blank Line separator, <400> field identifier
L:32 M:283 W: Missing Blank Line separator, <220> field identifier
L:37 M:283 W: Missing Blank Line separator, <400> field identifier
L:44 M:283 W: Missing Blank Line separator, <220> field identifier
L:45 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:48 M:283 W: Missing Blank Line separator, <400> field identifier
L:55 M:283 W: Missing Blank Line separator, <220> field identifier
L:56 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:59 M:283 W: Missing Blank Line separator, <400> field identifier
L:67 M:283 W: Missing Blank Line separator, <220> field identifier
L:68 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:5
L:70 M:283 W: Missing Blank Line separator, <400> field identifier
L:78 M:283 W: Missing Blank Line separator, <220> field identifier
L:79 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:81 M:283 W: Missing Blank Line separator, <400> field identifier
L:89 M:283 W: Missing Blank Line separator, <220> field identifier
L:90 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:92 M:283 W: Missing Blank Line separator, <400> field identifier
L:99 M:283 W: Missing Blank Line separator, <220> field identifier
L:100 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:8
L:102 M:283 W: Missing Blank Line separator, <400> field identifier
L:109 M:283 W: Missing Blank Line separator, <220> field identifier
L:112 M:283 W: Missing Blank Line separator, <400> field identifier
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L:145 M:283 W: Missing Blank Line separator, <400> field identifier
L:155 M:283 W: Missing Blank Line separator, <220> field identifier
L:158 M:283 W: Missing Blank Line separator, <400> field identifier
L:214 M:283 W: Missing Blank Line separator, <220> field identifier
L:217 M:283 W: Missing Blank Line separator, <400> field identifier